From: **Cavan, Emma L** e.cavan@imperial.ac.uk
Subject: Re: [MRes] done: scripting autotroph and heterotroph models
Date: February 13, 2020 at 4:28 PM
To: Ho, Pok pok.ho19@imperial.ac.uk, Clegg, Tom t.clegg17@imperial.ac.uk

https://nbviewer.jupyter.org/github/CleggTom/Bacteria_EcoFunc/blob/master/notebooks/Metabolic_model.ipynb

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From: Ho, Pok <pok.ho19@imperial.ac.uk>
Sent: 13 February 2020 3:45 PM
To: Cavan, Emma L <e.cavan@imperial.ac.uk>
Subject: Re: [MRes] done: scripting autotroph and heterotroph models

Dear Emma,

I'm sorry that my lecture has still not ended.
I'll be here right after the end of the lecture

Sorry,
PokMan

> On Feb 13, 2020, at 2:17 PM, Cavan, Emma L <e.cavan@imperial.ac.uk> wrote:
>
> Also, see a list of models NPZ (nutrient phytoplankton zooplankton) which also have D (detritus) and B (bacteria). Those listed as NPZDB will have some kind of coupling between phytoplankton and bacteria.
>
> The table comes from this paper https://www.geosci-model-dev.net/8/2231/2015/
>
> From: Cavan, Emma L <e.cavan@imperial.ac.uk>
> Sent: 13 February 2020 2:12 PM
> To: Ho, Pok <pok.ho19@imperial.ac.uk>
> Cc: Rosindell, James L <j.rosindell@imperial.ac.uk>; Pawar, Samraat <s.pawar@imperial.ac.uk>; Clegg, Tom <t.clegg17@imperial.ac.uk>
> Subject: Re: [MRes] done: scripting autotroph and heterotroph models
>
> The office im in opposite samraats will be good.
>
> Tom - are you coming?
>
> Emma
> From: Ho, Pok <pok.ho19@imperial.ac.uk>
> Sent: 13 February 2020 12:27 PM
> To: Cavan, Emma L <e.cavan@imperial.ac.uk>
> Cc: Rosindell, James L <j.rosindell@imperial.ac.uk>; Pawar, Samraat <s.pawar@imperial.ac.uk>; Clegg, Tom <t.clegg17@imperial.ac.uk>
> Subject: Re: [MRes] done: scripting autotroph and heterotroph models
>
> Dear Emma,
> Where would you prefer for our meeting at 15:30 today?
> Best,
> PokMan

>
> > On Feb 13, 2020, at 10:01 AM, Cavan, Emma L <e.cavan@imperial.ac.uk> wrote:
> >
> > Thanks PokMan, yes I will be there at 330 today.
> >
> >
> > Emma
> > From: Ho, Pok <pok.ho19@imperial.ac.uk>
> > Sent: 12 February 2020 6:35 PM
> > To: Rosindell, James L <j.rosindell@imperial.ac.uk>; Pawar, Samraat <s.pawar@imperial.ac.uk>; Cavan, Emma L <e.cavan@imperial.ac.uk>; Clegg, Tom <t.clegg17@imperial.ac.uk>
> > Subject: [MRes] done: scripting autotroph and heterotroph models
> >
> > Dear all,
> >
> > Using the same Jupyter notebook <https://nbviewer.jupyter.org/github/ph-u/Project/blob/master/sandbox/m_autophototroph.ipynb>, I have scripted both the autotroph and heterotroph models.
> >
> > The heterotroph model is from the paper (suggested by Samraat) below:
> > Marsland, R. et al. Available energy fluxes drive a transition in the diversity, stability, and functional structure of microbial communities. PLoS Comput. Biol. 15, e1006793 (2019).
> >
> > One interesting thing I discovered is the heterotroph model has no carrying capacity for the consumer, which has made the curve super unstable if it is the only consumer in the system. Food source in that model is monitored by another competing species but those terms are not applicable in my current model. So under no competition and no carrying capacity to suppress the consumer, the model cannot limit the consumer population.
> >
> > Tomorrow I will be meeting Samraat for this project. Emma and Tom, will you also join this meeting?
> >
> > Best,
> > PokMan
>
> <Screenshot 2020-02-13 at 14.14.01.png>